

ALIGNMENT

LOCUS STMAFSAA 1203 bp DNA linear BCT 26-APR-1993
 DEFINITION S.griseus afsA gene encoding a possible A-factor biosynthesis protein.
 ACCESSION M24250
 VERSION M24250.1 GI:153148
 KEYWORDS A-factor biosynthesis.
 SOURCE Streptomyces griseus
 ORGANISM Streptomyces griseus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (bases 1 to 1203)
 AUTHORS Horinouchi,S., Suzuki,H., Nishiyama,M. and Beppu,T.
 TITLE Nucleotide sequence and transcriptional analysis of the Streptomyces griseus gene (afsA) responsible for A-factor biosynthesis
 JOURNAL J. Bacteriol. 171 (2), 1206-1210 (1989)
 COMMENT Original source text: S.griseus DNA.

Alignment Scores:

Pred. No.:	7.91e-56	Length:	1203
Score:	1050.50	Matches:	201
Percent Similarity:	73.57%	Conservative:	30
Best Local Similarity:	64.01%	Mismatches:	82
Query Match:	63.86%	Indels:	1
DB:	1	Gaps:	1

US-10-017-471B-17 (1-313) x STMAFSAA (1-1203)

Qy	1	MetProGluAlaValValLeuIleAsnSerAlaSerAspAlaAsnSerIleGluGlnThr	20
Db	165	ATGCCCAGCAGCAGTCTTGATCGATCCGGTGCCGACTATGGACGCGGAGGCCGAGGTG	224
Qy	21	AlaLeuProValProMetAlaLeuValHisArgThrArgValGlnAspAlaPheProVal	40
Db	225	GTGCATCCCGTGCGGATCGAGATGGTGACCCGACCGAGGCCGAGGACGCCTTTCCGCGC	284
Qy	41	SerTrpIleProLysGlyGlyAspArgPheSerValThrAlaValLeuProHisAspHis	60
Db	285	AACTGGGTACGCCTGGGGCGCGACCGGTTGCGGGTGAAGCGGTCCTTCCGCACGACCAT	344
Qy	61	ProPhePheAlaProValHisGlyAspArgHisAspProLeuLeuIleAlaGluThrLeu	80
Db	345	CCCTTCTTCGCTCCGGTGCGGTGACGACCTGCACGATCCGCTGCTGGTCCGCGAGGCCATG	404
Qy	81	ArgGlnAlaAlaMetLeuValPheHisAlaGlyTyrGlyValProValGlyTyrHisPhe	100
Db	405	CGGCAGGCGGCCATGCTCGCCTTCCACGCGGGTACGGGATCCCGCTCGGCTACCACTTC	464
Qy	101	LeuMetThr---LeuAspTyrThrCysHisLeuAspHisLeuGlyValSerGlyGluVal	119
Db	465	CTCCTGACGGAGCTGGACTACGTCTGCCATCCCGAGCACCTCGGCGTGGGGGGCGAGCCC	524
Qy	120	AlaGluLeuGluValGluValAlaCysSerGlnLeuLysPheArgGlyGlyGlnProVal	139
Db	525	ACCGAGATCGGCCTGGAGGTGTTCTGCTCCGACCTGAAGTGGCGGGCCGGGCTCCCGGCG	584

Qy 140 GlnGlyGlnValAspTrpAlaValArgArgAlaGlyArgLeuAlaAlaThrGlyThrAla 159
 |||||:::| | | | | | | | | | | | | | | | | | | | |
 Db 585 CAGGGGCGCGTCGGCTGGGCGGTGCACCGGGGCGACCGGCTCGCCGCGACGGGGGTGGCG 644
 Qy 160 ThrThrArgPheThrSerProGlnValTyrArgArgMetArgGlyAspPheAlaThrPro 179
 |||||:::| | | | | | | | | | | | | | | | | | | | |
 Db 645 GCGACCCGGTTTCAGCACGCCCAAGGCCTACCGGCGGATGCGCGGTGACGTCCCGGTTCGAG 704
 Qy 180 ThrAlaSerValProGlyThrAlaProValProAlaAlaArgAlaGlyArgThrArgAsp 199
 |||:::| | | | | | | | | | | | | | | | | | | | |
 Db 705 GGCATATCCCTACCGGAGACCGCGCCGGTCCCGGCCTCGCCGCGGGCCGCGCCCGCGTC 764
 Qy 200 GluAspValValLeuSerAlaSerSerGlnGlnAspThrTrpArgLeuArgValAspThr 219
 ||||| | | | | | | | | | | | | | | | | | | | | |
 Db 765 GAGGACGTGGTGCTCTCGGGACGGGGCGGGAGGAGTCTGGGAAGTGC GCGTGGACACC 824
 Qy 220 SerHisProThrLeuPheGlnArgProAsnAspHisValProGlyMetLeuLeuLeuGlu 239
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 825 CGGCATCCGACCCTCTTCCAGCGCCCCAACGACCACGTCCCGGGCATGCTCCTGCTGGAG 884
 Qy 240 AlaAlaArgGlnAlaAlaCysLeuValThrGlyProAlaProPheValProSerIleGly 259
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 885 GCGGCCCGTCAGGCCGCGTGCCTGGTGGCGGGCCCGCGGAATCGTTCCGGTGGAGGCG 944
 Qy 260 GlyThrArgPheValArgTyrAlaGluPheAspSerProCysTrpIleGlnAlaThrVal 279
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 945 CGCACCCGGTTCCACCGGTACTCCGAGTTCGGCAGCCCGTGCTGGATAGGGGCGGTGGTC 1004
 Qy 280 ArgProGlyProAlaAlaGlyLeuThrThrValArgValThrGlyHisGlnAspGlySer 299
 ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1005 CAGCCGGGGGCGGACGAGGATACGGTGACCGTCCGGTGACAGGCCATCAGGACGGCGAG 1064
 Qy 300 LeuValPheLeuThrThrLeuSerGlyProAlaPheSerGly 313
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1065 ACGGTCTTCTCCACGGTCCTGTCCGGCCCCCGGGCCACGGC 1106

LOCUS AB001608 1215 bp DNA linear BCT 22-NOV-1997
 DEFINITION Streptomyces virginiae DNA for BarX, complete cds.
 ACCESSION AB001608
 VERSION AB001608.1 GI:2641955
 KEYWORDS BarX.
 SOURCE Streptomyces virginiae
 ORGANISM Streptomyces virginiae
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.
 REFERENCE 1 (sites)
 AUTHORS Kinoshita,H., Ipposhi,H., Okamoto,S., Nakano,H., Nihira,T. and Yamada,Y.
 TITLE Butyrolactone autoregulator receptor protein (BarA) as a transcriptional regulator in Streptomyces virginiae
 JOURNAL J. Bacteriol. 179 (22), 6986-6993 (1997)
 REFERENCE 2 (bases 1 to 1215)
 AUTHORS Kinoshita,H.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-1997) Hiroshi Kinoshita, Osaka University, Department of Engineering; Yamadaoka 2-1, Suita, Osaka 565, Japan (E-mail:kinosita@biochem.bio.eng.osaka-u.ac.jp, Tel:+81-6-879-7433, Fax:+81-6-879-7432)

Alignment Scores:

Pred. No.:	5.99e-26	Length:	1215
Score:	562.50	Matches:	126
Percent Similarity:	56.12%	Conservative:	39
Best Local Similarity:	42.86%	Mismatches:	118
Query Match:	34.19%	Indels:	11
DB:	1	Gaps:	3

US-10-017-471B-17 (1-313) x AB001608 (1-1215)

Qy	19	GlnThrAlaLeuPro-----ValProMetAlaLeuVal	29
Db	214	CAGACCGGCCGACCGGCCCGCGCATCGGCCATGACCAGCACGGTTCGCGGGAGCTGGTC	273
Qy	30	HisArgThrArgValGlnAspAlaPheProValSerTrpIleProLysGlyGlyAspArg	49
		:: ::	
Db	274	CACCGGGCGCGGTCGCCGAAGTGTCTTGACGGGATGGAGCCGGACCGCGGAGAACCGA	333
Qy	50	PheSerValThrAlaValLeuProHisAspHisProPhePheAlaProValHisGlyAsp	69
		::: :: ::	
Db	334	TTCGCCCTGACGGCGCAGTGGCCCAGGGCGCACAGCTACTTCACCCCGGTGAACGGC---	390
Qy	70	ArgHisAspProLeuLeuIleAlaGluThrLeuArgGlnAlaAlaMetLeuValPheHis	89
		::: :: ::: :::	
Db	391	TGCTACGACCCGCTGCTGGCCTCCGAAACCATCCGACAGGTTCGGTACCCTTCTCTCCAC	450
Qy	90	AlaGlyTyrGlyValProValGlyTyrHisPheLeuMet---ThrLeuAspTyrThrCys	108
		::: :::::	
Db	451	GCGGAGTTCGGGGTCTCGTTCGGGGACAGTTCCTGATGTGGGACCTTCACCACAGCGTC	510
Qy	109	HisLeuAspHisLeuGlyValSerGlyGluValAlaGluLeuGluValGluValAlaCys	128
		::: ::: :::	
Db	511	AGGCCCCGAGCAGGCGGGCGTTCGGTCCCGCCCGCCGACCTGGAAGTGGACGTCATCTGT	570

Qy	129	SerGlnLeuLysPheArgGlyGlyGlnProValGlnGlyGlnValAspTrpAlaValArg	148
		:::: :::	
Db	571	TCCGACATCCGCCCGCCGGCCGCCTGGCGGGCATGCGCTACGAGGTACCCTCTAC	630
Qy	149	ArgAlaGlyArgLeuAlaAlaThrGlyThrAlaThrThrArgPheThrSerProGlnVal	168
		:::	
Db	631	TGCGGGCGCCAGGTGATCGCCACCGGCGGCGCCGCTTCGACTGCACCAGCCCCGCCGTC	690
Qy	169	TyrArgArgMetArgGlyAspPheAlaThrProThrAlaSerValProGlyThrAlaPro	188
		::: :::	
Db	691	TACCAGCGGCTGCGCGGTGACCGGGTCGGTGCCACGGGCGTGC GGCCCC'TGCCGACGCCG	750
Qy	189	ValProAlaAlaArgAlaGlyArgThrArgAspGluAspValValLeuSerAlaSerSer	208
		:::	
Db	751	CTCGCCCCCGCGTCGGTCGGCCGCTTCCTCACCACGGACGTCGTCCTGTCCGCCACCGAG	810
Qy	209	GlnGlnAspThrTrpArgLeuArgValAspThrSerHisProThrLeuPheGlnArgPro	228
		::: :::	
Db	811	CGTCCGCTGGAGTTGGCAGCTGCGGGTGGACGAACAGCATCCC GTGCTCTTCGACCACCT	870
Qy	229	AsnAspHisValProGlyMetLeuLeuLeuGluAlaAlaArgGlnAlaAlaCysLeuVal	248
		::: ::: :::	
Db	871	GTCGACCACGTTCCCGGCATGGTGCTGATGGAGTCCGCCCCCAGGCCGCCAGGCCATC	930
Qy	249	ThrGlyProAlaProPheValProSerIleGlyGlyThrArgPheValArgTyrAlaGlu	268
		::: ::: :::	
Db	931	GACCCGTCCCGCCGTTCTCTGCCGACCAGATGCGCTCCGAGTTCAGCCGGTACGCGGAG	990
Qy	269	PheAspSerProCysTrpIleGlnAlaThrValArgProGlyProAlaAlaGlyLeuThr	288
Db	991	CTCGACAGGCCCTGCTGGATA CAGGCGGAGCCGCTGCCCGCGGCCGACAACGGCGACCGG	1050
Qy	289	ThrValArgValThrGlyHisGlnAspGlySerLeuValPhe	302
		:::	
Db	1051	CAGGTCCGCGTCAACGGCCACCAGGACGACACCACCGTCTTC	1092